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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/436,339ADATE: 07/02/98
TIME: 14:54:25

INPUT SET: S3203.raw

#19

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Papayannopoulou, Thalia (USA only)
6 Board of Regents, U.
7 Washington (except USA)
8
9 (ii) TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
10 CELLS
11
12 (iii) NUMBER OF SEQUENCES: 10
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: c/o FISH & NEAVE
16 (B) STREET: 1251 Avenue of the Americas
17 (C) CITY: New York
18 (D) STATE: New York
19 (E) COUNTRY: U.S.A.
20 (F) ZIP: 10020
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 08/436,339
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 08/463,128
35 (B) FILING DATE: 05-JUN-1995
36
37 (A) APPLICATION NUMBER: PCT/US93/11060
38 (B) FILING DATE: 11-11-1993
39
40 (A) APPLICATION NUMBER: US 07/977,702
41 (B) FILING DATE: 13-NOV-1992
42
43 (viii) ATTORNEY/AGENT INFORMATION:
44 (A) NAME: Haley Jr., James F.
45 (B) REGISTRATION NUMBER: 27,794
46 (C) REFERENCE/DOCKET NUMBER: B173CIP

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47
48 (ix) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: (212) 596-9000
50 (B) TELEFAX: (212) 596-9090
51
52
53 (2) INFORMATION FOR SEQ ID NO:1:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 360 base pairs
57 (B) TYPE: nucleic acid
58 (C) STRANDEDNESS: single
59 (D) TOPOLOGY: linear
60
61
62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65 GTCAAACCTGC AGCAGTCTGG GGCAGAGCTT GTGAAGCCAG GGGCCTCAGT CAAGTTGTCC 60
66
67 TGCACAGCTT CTGGCTTCAA CATTAAAGAC ACCTATATGC ACTGGGTGAA GCAGAGGCCT 120
68
69 GAACAGGGCC TGGAGTGGAT TGGAAGGATT GATCCTGCGA GTGGCGATAC TAAATATGAC 180
70
71 CCGAAGTTCC AGGTCAAGGC CACTATTACA GCGGACACGT CCTCCAACAC AGCCTGGCTG 240
72
73 CAGCTCAGCA GCCTGACATC TGAGGACACT GCCGTCTACT ACTGTGCAGA CGGAATGTGG 300
74
75 GTATCAACGG GATATGCTCT GGACTTCTGG GGCAAGGGA CCACGGTCAC CGTCTCCTCA 360
76
77
78 (2) INFORMATION FOR SEQ ID NO:2:
79
80 (i) SEQUENCE CHARACTERISTICS:
81 (A) LENGTH: 318 base pairs
82 (B) TYPE: nucleic acid
83 (C) STRANDEDNESS: single
84 (D) TOPOLOGY: linear
85
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
89
90 AGTATTGTGA TGACCCAGAC TCCCAAATTC CTGCTTGTTC CAGCAGGAGA CAGGGTTACC 60
91
92 ATAACCTGCA AGGCCAGTCA GAGTGTGACT AATGATGTAG CTTGGTACCA ACAGAAGCCA 120
93
94 GGGCAGTCTC CTAAACTGCT GATATATTAT GCATCCAATC GCTACACTGG AGTCCCTGAT 180
95
96 CGCTTCACTG GCAGTGGATA TGGGACGGAT TTCACTTTCA CCATCAGCAC TGTGCAGGCT 240
97
98 GAAGACCTGG CAGTTTATTT CTGTCAGCAG GATTATAGCT CTCCGTACAC GTTCGGAGGG 300
99

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318

100 GGGACCAAGC TGGAGATC

101

102 (2) INFORMATION FOR SEQ ID NO:3:

103

104 (i) SEQUENCE CHARACTERISTICS:

105 (A) LENGTH: 429 base pairs

106 (B) TYPE: nucleic acid

107 (C) STRANDEDNESS: single

108 (D) TOPOLOGY: linear

109

110

111 (ix) FEATURE:

112 (A) NAME/KEY: sig_peptide

113 (B) LOCATION: 1..57

114

115 (ix) FEATURE:

116 (A) NAME/KEY: mat_peptide

117 (B) LOCATION: 58..429

118

119 (ix) FEATURE:

120 (A) NAME/KEY: CDS

121 (B) LOCATION: 1..429

122

123 (ix) FEATURE:

124 (A) NAME/KEY: misc_feature

125 (B) LOCATION: 1

126 (D) OTHER INFORMATION: /note= "pMDR1019 insert: Stage 1
127 heavy chain variable region"

128

129

130 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

131

132 ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT 48
133 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
134 -19 -15 -10 -5

135

136 GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA 96
137 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
138 1 5 10

139

140 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GTG TCT GGC TTC AAC ATT 144
141 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile
142 15 20 25

143

144 AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT 192
145 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
146 30 35 40 45

147

148 GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC 240
149 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
150 50 55 60

151

152 CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC

288

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153 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
 154 65 70 75
 155
 156 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC 336
 157 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 158 80 85 90
 159
 160 TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC 384
 161 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
 162 95 100 105
 163
 164 TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429
 165 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
 166 110 115 120
 167
 168
 169 (2) INFORMATION FOR SEQ ID NO:4:
 170
 171 (i) SEQUENCE CHARACTERISTICS:
 172 (A) LENGTH: 143 amino acids
 173 (B) TYPE: amino acid
 174 (D) TOPOLOGY: linear
 175
 176 (ii) MOLECULE TYPE: protein
 177
 178 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
 179
 180 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
 181 -19 -15 -10 -5
 182
 183 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
 184 1 5 10
 185
 186 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Asn Ile
 187 15 20 25
 188
 189 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
 190 30 35 40 45
 191
 192 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
 193 50 55 60
 194
 195 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn
 196 65 70 75
 197
 198 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 199 80 85 90
 200
 201 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
 202 95 100 105
 203
 204 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
 205 110 115 120

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206
 207 (2) INFORMATION FOR SEQ ID NO:5:
 208
 209 (i) SEQUENCE CHARACTERISTICS:
 210 (A) LENGTH: 386 base pairs
 211 (B) TYPE: nucleic acid
 212 (C) STRANDEDNESS: single
 213 (D) TOPOLOGY: linear
 214
 215
 216 (ix) FEATURE:
 217 (A) NAME/KEY: sig_peptide
 218 (B) LOCATION: 1..57
 219
 220 (ix) FEATURE:
 221 (A) NAME/KEY: mat_peptide
 222 (B) LOCATION: 58..384
 223
 224 (ix) FEATURE:
 225 (A) NAME/KEY: CDS
 226 (B) LOCATION: 1..384
 227
 228 (ix) FEATURE:
 229 (A) NAME/KEY: misc_feature
 230 (B) LOCATION: 1
 231 (D) OTHER INFORMATION: /note= "pBag190 insert: VK1 (DQL)
 232 light chain variable region"
 233
 234
 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 236
 237 ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GCT ACC GCT ACC GGT 48
 238 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 239 -19 -15 -10 -5
 240
 241 GTT CAC TCC GAC ATC CAG CTG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
 242 Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
 243 1 5 10
 244
 245 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG 144
 246 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
 247 15 20 25
 248
 249 ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG 192
 250 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 251 30 35 40 45
 252
 253 CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA AGC AGA 240
 254 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
 255 50 55 60
 256
 257 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288
 258 Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

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SEQUENCE VERIFICATION REPORT
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Original Text